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RAW SEQUENCE LISTING
PATENT APPLICATION: US/10/006,852

DATE: 07/18/2002
TIME: 11:21:10

Input Set : A:\Kinnersley Seq. List.txt
Output Set: N:\CRF3\07182002\J006852.raw

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C--> 3 <110> APPLICANT: Kinnersley, Alan M.
      4 Turano, Frank J.
      6 <120> TITLE OF INVENTION: Methods for Regulating Plant GABA Production
      8 <130> FILE REFERENCE: 7224-65
C--> 10 <140> CURRENT APPLICATION NUMBER: US/10/006,852
C--> 10 <141> CURRENT FILING DATE: 2002-07-01
      11 <150> PRIOR APPLICATION NUMBER: US 60/246,367
      11 <151> PRIOR FILING DATE: 2000-11-07
      13 <160> NUMBER OF SEQ ID NOS: 24
      15 <170> SOFTWARE: Patentin version 3.1
      17 <210> SEQ ID NO: 1
      18 <211> LENGTH: 1509
      19 <212> TYPE: DNA
      20 <213> ORGANISM: Arabidopsis thaliana
      22 <220> FEATURE:
      23 <221> NAME/KEY: CDS
      24 <222> LOCATION: (1)..(1509)
      25 <223> OTHER INFORMATION:
      28 <400> SEQUENCE: 1
      29 atg gtg ctc tcc cac gcc gac gta tcg gag tcg gac gtc tcc gtc cac tcc 48
      30 Met Val Leu Ser His Ala Val Ser Glu Ser Asp Val Ser Val His Ser
      31 1 5 10 15
      33 aca ttc gca tca cgt tac gtc cgt act tca ctt cct agg ttc aag atg 96
      34 Thr Phe Ala Ser Arg Tyr Val Arg Thr Ser Leu Pro Arg Phe Lys Met
      35 20 25 30
      37 ccg gaa aac tcg att cct aag gaa gcg gcg tat cag atc atc aac gac 144
      38 Pro Glu Asn Ser Ile Pro Lys Glu Ala Ala Tyr Gln Ile Ile Asn Asp
      39 35 40 45
      41 gag ctg atg ctt gac ggg aat cca cgg ttg aac tta gcc tcc ttt gtg 192
      42 Glu Leu Met Leu Asp Gly Asn Pro Arg Leu Asn Leu Ala Ser Phe Val
      43 50 55 60
      45 acg aca tgg atg gag cct gag tgt gat aaa ctc atc atg tcc tcc atc 240
      46 Thr Thr Trp Met Glu Pro Glu Cys Asp Lys Leu Ile Met Ser Ser Ile
      47 65 70 75 80
      49 aac aag aac tat gtt gac atg gac gag tac ccc gtc acc acc gaa ctt 288
      50 Asn Lys Asn Tyr Val Asp Met Asp Glu Tyr Pro Val Thr Thr Glu Leu
      51 85 90 95
      53 cag aac cga tgt gtg aac atg att gca cat cta ttc aat gca ccg tta 336
      54 Gln Asn Arg Cys Val Asn Met Ile Ala His Leu Phe Asn Ala Pro Leu
      55 100 105 110
      57 gaa gag gcg gag acc gcc gtc gga gta gga acc gtt gga tca tcg gag 384
      58 Glu Glu Ala Glu Thr Ala Val Gly Val Gly Thr Val Gly Ser Ser Glu
      59 115 120 125
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61 gcc ata atg ttg gcc ggt ttg gcc ttc aag cgt aaa tgg cag aac aag      432
62 Ala Ile Met Leu Ala Gly Leu Ala Phe Lys Arg Lys Trp Gln Asn Lys
63 130 135
65 cgc aaa gct gaa ggc aaa ccc gtc gat aaa ccc aac att gtc acc gga      480
66 Arg Lys Ala Glu Gly Lys Pro Val Asp Lys Pro Asn Ile Val Thr Gly
67 145 150 155 160
69 gcc aat gtt caa gtg tgt tgg gag aaa ttc gct agg tac ttt gag gtt      528
70 Ala Asn Val Gln Val Cys Trp Glu Lys Phe Ala Arg Tyr Phe Glu Val
71 165 170 175
73 gaa ctt aag gaa gtg aaa ttg agt gaa gga tac tat gtg atg gac cct      576
74 Glu Leu Lys Glu Val Lys Leu Ser Glu Gly Tyr Tyr Val Met Asp Pro
75 180 185 190
77 caa caa gct gtt gat atg gtt gat gag aac acc att tgt gtt gcg gac      624
78 Gln Gln Ala Val Asp Met Val Asp Glu Asn Thr Ile Cys Val Ala Asp
79 195 200 205
81 att ctt ggt tcc act ctt aat gga gaa ttc gaa gat gtt aaa ctc ttg      672
82 Ile Leu Gly Ser Thr Leu Asn Gly Glu Phe Glu Asp Val Lys Leu Leu
83 210 215 220
85 aac gat ctc ttg gtc gaa aag aac aaa gaa acc gga tgg gat aca cca      720
86 Asn Asp Leu Leu Val Glu Lys Asn Lys Glu Thr Gly Trp Asp Thr Pro
87 225 230 235 240
89 atc cac gtg gat gcg gca agt gga gga ttc att gca ccg ttt ttg tat      768
90 Ile His Val Asp Ala Ala Ser Gly Gly Phe Ile Ala Pro Phe Leu Tyr
91 245 250 255
93 cgc gaa ttg gaa tgg gac ttt aga ctt ccc ttg gtg aag agt atc aat      816
94 Pro Glu Leu Glu Trp Asp Phe Arg Leu Pro Leu Val Lys Ser Ile Asn
95 260 265 270
97 gtg agt ggt cac aag tat gga ctt gtg tac gca ggg att ggt tgg gtg      864
98 Val Ser Gly His Lys Tyr Gly Leu Val Tyr Ala Gly Ile Gly Trp Val
99 275 280 285
101 atc tgg aga aac aaa gag gat ttg cct gag gaa ctc atc ttc cat atc      912
102 Ile Trp Arg Asn Lys Glu Asp Leu Pro Glu Glu Leu Ile Phe His Ile
103 290 295 300
105 aat tat ctt ggt gct gac caa ccc acc ttt act ctc aat ttc tcc aaa      960
106 Asn Tyr Leu Gly Ala Asp Gln Pro Thr Phe Thr Leu Asn Phe Ser Lys
107 305 310 315 320
109 ggt tca agt caa gtc att gct caa tac tac caa ctt atc cga ttg ggc      1008
110 Gly Ser Ser Gln Val Ile Ala Gln Tyr Tyr Gln Leu Ile Arg Leu Gly
111 325 330 335
113 cac gag ggt tac aga aat gtg atg gag aat tgc aga gag aat atg atc      1056
114 His Glu Gly Tyr Arg Asn Val Met Glu Asn Cys Arg Glu Asn Met Ile
115 340 345 350
117 gtc cta agg gaa gga ctt gag aag aca gaa agg ttc aac atc gtc tca      1104
118 Val Leu Arg Glu Gly Leu Glu Lys Thr Glu Arg Phe Asn Ile Val Ser
119 355 360 365
121 aag gac gag gga gtg cca ctt gtc gct ttc tcc ttg aaa gat agc agc      1152
122 Lys Asp Glu Gly Val Pro Leu Val Ala Phe Ser Leu Lys Asp Ser Ser
123 370 375 380
125 tgt cac act gag ttc gaa atc tcc gac atg ctt cgc agg tat gga tgg      1200

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126 Cys His Thr Glu Phe Glu Ile Ser Asp Met Leu Arg Arg Tyr Gly Trp
127 385                               390           395           400
129 ata gtg cgc gcc tac aca atg cct cca aat gca caa cac atc act gtt      1248
130 Ile Val Pro Ala Tyr Thr Met Pro Pro Asn Ala Gln His Ile Thr Val
131                               405           410           415
133 ctt cgt gtg gtt atc aga gaa gat ttc tcg aga aca ctc gct gag aga      1296
134 Leu Arg Val Val Ile Arg Glu Asp Phe Ser Arg Thr Leu Ala Glu Arg
135                               420           425           430
137 ctt gtg atc gat ata gag aaa gtg atg cgt gag ctc gat gag ctt cct      1344
138 Leu Val Ile Asp Ile Glu Lys Val Met Arg Glu Leu Asp Glu Leu Pro
139                               435           440           445
141 tcg aga gtg att cac aaa ata tca ctt gga caa gag aag agt gaa tct      1392
142 Ser Arg Val Ile His Lys Ile Ser Leu Gly Gln Glu Lys Ser Glu Ser
143                               450           455           460
145 aac agc gat aac ttg atg gtc acg gtg aag aag agc gat atc gac aag      1440
146 Asn Ser Asp Asn Leu Met Val Thr Val Lys Lys Ser Asp Ile Asp Lys
147 465                               470           475           480
149 cag aga gat atc atc act gcc tgg aag aag ttt gtc gcc gac agg aag      1488
150 Gln Arg Asp Ile Ile Thr Gly Trp Lys Lys Phe Val Ala Asp Arg Lys
151                               485           490           495
153 aag acg agt ggt atc tgc taa      1509
154 Lys Thr Ser Ser Gly Ile Cys
155                               500
158 <210> SEQ ID NO: 2
159 <211> LENGTH: 502
160 <212> TYPE: PRT
161 <213> ORGANISM: Arabidopsis thaliana
163 <400> SEQUENCE: 2
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166 1                               5           10           15
169 Thr Phe Ala Ser Arg Tyr Val Arg Thr Ser Leu Pro Arg Phe Lys Met
170                               20           25           30
173 Pro Glu Asn Ser Ile Pro Lys Glu Ala Ala Tyr Gln Ile Ile Asn Asp
174                               35           40           45
177 Glu Leu Met Leu Asp Gly Asn Pro Arg Leu Asn Leu Ala Ser Phe Val
178                               50           55           60
181 Thr Thr Trp Met Glu Pro Glu Cys Asp Lys Leu Ile Met Ser Ser Ile
182 65                               70           75           80
185 Asn Lys Asn Tyr Val Asp Met Asp Glu Tyr Pro Val Thr Thr Glu Leu
186                               85           90           95
189 Gln Asn Arg Cys Val Asn Met Ile Ala His Leu Phe Asn Ala Pro Leu
190                               100          105          110
193 Glu Glu Ala Glu Thr Ala Val Gly Val Gly Thr Val Gly Ser Ser Glu
194                               115          120          125
197 Ala Ile Met Leu Ala Gly Leu Ala Phe Lys Arg Lys Trp Gln Asn Lys
198                               130          135          140
201 Arg Lys Ala Glu Gly Lys Pro Val Asp Lys Pro Asn Ile Val Thr Gly
202 145                               150          155          160
205 Ala Asn Val Gln Val Cys Trp Glu Lys Phe Ala Arg Tyr Phe Glu Val

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206                               165                               170                               175
209 Glu Leu Lys Glu Val Lys Leu Ser Glu Gly Tyr Tyr Val Met Asp Pro
210                               180                               185                               190
213 Gln Gln Ala Val Asp Met Val Asp Glu Asn Thr Ile Cys Val Ala Asp
214                               195                               200                               205
217 Ile Leu Gly Ser Thr Leu Asn Gly Glu Phe Glu Asp Val Lys Leu Leu
218                               210                               215                               220
221 Asn Asp Leu Leu Val Glu Lys Asn Lys Glu Thr Gly Trp Asp Thr Pro
222 225                               230                               235                               240
225 Ile His Val Asp Ala Ala Ser Gly Gly Phe Ile Ala Pro Phe Leu Tyr
226                               245                               250                               255
229 Pro Glu Leu Glu Trp Asp Phe Arg Leu Pro Leu Val Lys Ser Ile Asn
230                               260                               265                               270
233 Val Ser Gly His Lys Tyr Gly Leu Val Tyr Ala Gly Ile Gly Trp Val
234                               275                               280                               285
237 Ile Trp Arg Asn Lys Glu Asp Leu Pro Glu Glu Leu Ile Phe His Ile
238                               290                               295                               300
241 Asn Tyr Leu Gly Ala Asp Gln Pro Thr Phe Thr Leu Asn Phe Ser Lys
242 305                               310                               315                               320
245 Gly Ser Ser Gln Val Ile Ala Gln Tyr Tyr Gln Leu Ile Arg Leu Gly
246                               325                               330                               335
249 His Glu Gly Tyr Arg Asn Val Met Glu Asn Cys Arg Glu Asn Met Ile
250                               340                               345                               350
253 Val Leu Arg Glu Gly Leu Glu Lys Thr Glu Arg Phe Asn Ile Val Ser
254                               355                               360                               365
257 Lys Asp Glu Gly Val Pro Leu Val Ala Phe Ser Leu Lys Asp Ser Ser
258                               370                               375                               380
261 Cys His Thr Glu Phe Glu Ile Ser Asp Met Leu Arg Arg Tyr Gly Trp
262 385                               390                               395                               400
265 Ile Val Pro Ala Tyr Thr Met Pro Pro Asn Ala Gln His Ile Thr Val
266                               405                               410                               415
269 Leu Arg Val Val Ile Arg Glu Asp Phe Ser Arg Thr Leu Ala Glu Arg
270                               420                               425                               430
273 Leu Val Ile Asp Ile Glu Lys Val Met Arg Glu Leu Asp Glu Leu Pro
274                               435                               440                               445
277 Ser Arg Val Ile His Lys Ile Ser Leu Gly Gln Glu Lys Ser Glu Ser
278                               450                               455                               460
281 Asn Ser Asp Asn Leu Met Val Thr Val Lys Lys Ser Asp Ile Asp Lys
282 465                               470                               475                               480
285 Gln Arg Asp Ile Ile Thr Gly Trp Lys Lys Phe Val Ala Asp Arg Lys
286                               485                               490                               495
289 Lys Thr Ser Gly Ile Cys
290                               500
293 <210> SEQ ID NO: 3
294 <211> LENGTH: 1665
295 <212> TYPE: DNA
296 <213> ORGANISM: Arabidopsis thaliana
298 <220> FEATURE:
299 <221> NAME/KEY: CDS

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300 <222> LOCATION: (17)..(1498)
301 <223> OTHER INFORMATION:
304 <400> SEQUENCE: 3
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306          Met Val Leu Thr Lys Thr Ala Thr Asn Asp Glu Ser
307          1          5          10
309 gtc tgc acc atg ttc gga tct cgc tat gtt cgc act aca ctt ccc aag      100
310 Val Cys Thr Met Phe Gly Ser Arg Tyr Val Arg Thr Thr Pro Lys
311          15          20          25
313 tat gag att ggt gag aat tcg ata ccg aaa gac gct gca tat cag atc      148
314 Tyr Glu Ile Gly Glu Asn Ser Ile Pro Lys Asp Ala Ala Tyr Gln Ile
315          30          35          40
317 ata aaa gat gag ctg atg ctt gat ggt aac ccg agg ctt aac cta gct      196
318 Ile Lys Asp Glu Leu Met Leu Asp Gly Asn Pro Arg Leu Asn Leu Ala
319          45          50          55          60
321 tcg ttt gtg act aca tgg atg gaa cca gag tgt gac aaa ctc atc atg      244
322 Ser Phe Val Thr Thr Trp Met Glu Pro Glu Cys Asp Lys Leu Ile Met
323          65          70          75
325 gac tct atc aac aag aac tac gtt gat atg gat gag tac cct gtc aca      292
326 Asp Ser Ile Asn Lys Asn Tyr Val Asp Met Asp Glu Tyr Pro Val Thr
327          80          85          90
329 act gag ctc cag aac cga tgt gta aac att ata gct cga ctg ttc aat      340
330 Thr Glu Leu Gln Asn Arg Cys Val Asn Ile Ile Ala Arg Leu Phe Asn
331          95          100          105
333 gcg cca ctc gag gaa tct gag acg gcg gtg gga gta ggg aca gtt ggt      388
334 Ala Pro Leu Glu Glu Ser Glu Thr Ala Val Gly Val Gly Thr Val Gly
335          110          115          120
337 tct tca gaa gcc atc atg tta gcc gga ttg gcc ttc aaa aga aaa tgg      436
338 Ser Ser Glu Ala Ile Met Leu Ala Gly Leu Ala Phe Lys Arg Lys Trp
339          125          130          135          140
341 cag aac aaa cgc aag gct gag ggt aaa ccc tat gac aaa ccc aac att      484
342 Gln Asn Lys Arg Lys Ala Glu Gly Lys Pro Tyr Asp Lys Pro Asn Ile
343          145          150          155
345 gtc act gga gcc aat gtt caa gtt tgc tgg gag aaa ttc gct cgg tac      532
346 Val Thr Gly Ala Asn Val Gln Val Cys Trp Glu Lys Phe Ala Arg Tyr
347          160          165          170
349 ttc gag gtg gag cta aag gaa gta aac cta agt gaa ggt tac tac gtg      580
350 Phe Glu Val Glu Leu Lys Glu Val Asn Leu Ser Glu Gly Tyr Tyr Val
351          175          180          185
353 atg gat cca gac aaa gca gca gaa atg gta gac gag aac aca atc tgt      628
354 Met Asp Pro Asp Lys Ala Ala Glu Met Val Asp Glu Asn Thr Ile Cys
355          190          195          200
357 gtc gca gcc ata ttg gga tcc aca ctc aac ggt gag ttc gaa gac gtg      676
358 Val Ala Ala Ile Leu Gly Ser Thr Leu Asn Gly Glu Phe Glu Asp Val
359          205          210          215          220
361 aaa cgt ctc aat gac ttg cta gtc aag aaa aac gag gag act ggt tgg      724
362 Lys Arg Leu Asn Asp Leu Leu Val Lys Lys Asn Glu Glu Thr Gly Trp
363          225          230          235
365 aac aca ccg atc cac gtg gat gca gca agt gga ggg ttc ata gct ccg      772

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VERIFICATION SUMMARY

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Input Set : A:\Kinnersley Seq. List.txt

Output Set: N:\CRF3\07182002\J006852.raw

L:10 M:270 C: Current Application Number differs, Replaced Current Application No

L:10 M:271 C: Current Filing Date differs, Replaced Current Filing Date